Paul Marjoram

List of Publications by Citations

48 papers	**5,013** citations
24 h-index	**49** g-index
49 ext. papers	**5,780** ext. citations
7.4 avg, IF	**5.07** L-index

#	Paper	IF	Citations
48	Genome-wide association study of 107 phenotypes in Arabidopsis thaliana inbred lines. *Nature*, **2010**, 465, 627-31	50.4	1257
47	Markov chain Monte Carlo without likelihoods. *Proceedings of the National Academy of Sciences of the United States of America*, **2003**, 100, 15324-8	11.5	672
46	A Big Bang model of human colorectal tumor growth. *Nature Genetics*, **2015**, 47, 209-16	36.3	646
45	An Arabidopsis example of association mapping in structured samples. *PLoS Genetics*, **2007**, 3, e4	6	537
44	Genome-wide association mapping in Arabidopsis identifies previously known flowering time and pathogen resistance genes. *PLoS Genetics*, **2005**, 1, e60	6	337
43	Fast and flexible simulation of DNA sequence data. *Genome Research*, **2009**, 19, 136-42	9.7	267
42	Modern computational approaches for analysing molecular genetic variation data. *Nature Reviews Genetics*, **2006**, 7, 759-70	30.1	156
41	Fast "coalescent" simulation. *BMC Genetics*, **2006**, 7, 16	2.6	155
40	Approximately sufficient statistics and bayesian computation. *Statistical Applications in Genetics and Molecular Biology*, **2008**, 7, Article26	1.2	125
39	Inferring clonal expansion and cancer stem cell dynamics from DNA methylation patterns in colorectal cancers. *Proceedings of the National Academy of Sciences of the United States of America*, **2009**, 106, 4828-33	11.5	108
38	Fine-scale mapping of disease genes with multiple mutations via spatial clustering techniques. *American Journal of Human Genetics*, **2003**, 73, 1368-84	11	84
37	Haplotype structure and phenotypic associations in the chromosomal regions surrounding two Arabidopsis thaliana flowering time loci. *Genetics*, **2004**, 168, 1627-38	4	63
36	A multigene expression panel for the molecular diagnosis of Barrett's esophagus and Barrett's adenocarcinoma of the esophagus. *Oncogene*, **2004**, 23, 4780-8	9.2	61
35	Critical role of nuclear calcium/calmodulin-dependent protein kinase IIdeltaB in cardiomyocyte survival in cardiomyopathy. *Journal of Biological Chemistry*, **2009**, 284, 24857-68	5.4	49
34	Estimating the rate of gene conversion on human chromosome 21. *American Journal of Human Genetics*, **2004**, 75, 386-97	11	41
33	Brief episode of ischemia activates protective genetic program in rat heart: a gene chip study. *Cardiovascular Research*, **2003**, 59, 450-9	9.9	40
32	Application of Bayesian spatial statistical methods to analysis of haplotypes effects and gene mapping. *Genetic Epidemiology*, **2003**, 25, 95-105	2.6	39

31	Exploring population genetic models with recombination using efficient forward-time simulations. *Genetics*, **2008**, 178, 2417-27	4	38
30	Age-related changes of cardiac gene expression following myocardial ischemia/reperfusion. *Archives of Biochemistry and Biophysics*, **2003**, 420, 268-78	4.1	34
29	The molecular signature of normal squamous esophageal epithelium identifies the presence of a field effect and can discriminate between patients with Barrett's esophagus and patients with Barrett's-associated adenocarcinoma. *Cancer Epidemiology Biomarkers and Prevention*, **2005**, 14, 2113-7	4	31
28	Association mapping with single-feature polymorphisms. *Genetics*, **2006**, 173, 1125-33	4	28
27	Estimating recombination rates from single-nucleotide polymorphisms using summary statistics. *Genetics*, **2006**, 174, 1517-28	4	26
26	The effects of rate variation on ancestral inference in the coalescent. *Genetics*, **2000**, 156, 1427-36	4	26
25	Many colorectal cancers are "flat" clonal expansions. *Cell Cycle*, **2009**, 8, 2187-93	4.7	24
24	Many private mutations originate from the first few divisions of a human colorectal adenoma. *Journal of Pathology*, **2015**, 237, 355-62	9.4	22
23	The age of a unique event polymorphism. *Genetics*, **2000**, 156, 401-9	4	19
22	High DNA methylation pattern intratumoral diversity implies weak selection in many human colorectal cancers. *PLoS ONE*, **2011**, 6, e21657	3.7	18
21	Choice of summary statistic weights in approximate Bayesian computation. *Statistical Applications in Genetics and Molecular Biology*, **2011**, 10,	1.2	14
20	Social effects for locomotion vary between environments in Drosophila melanogaster females. *Evolution; International Journal of Organic Evolution*, **2017**, 71, 1765-1775	3.8	13
19	A Bayesian Approach to Social Structure Uncovers Cryptic Regulation of Group Dynamics in Drosophila melanogaster. *American Naturalist*, **2015**, 185, 797-808	3.7	10
18	Using DNA methylation patterns to infer tumor ancestry. *PLoS ONE*, **2010**, 5, e12002	3.7	10
17	WhoGEM: an admixture-based prediction machine accurately predicts quantitative functional traits in plants. *Genome Biology*, **2019**, 20, 106	18.3	7
16	Inferring population parameters from single-feature polymorphism data. *Genetics*, **2006**, 173, 2257-67	4	7
15	Approximation Bayesian Computation **2013**, 1, 853		7
14	Ancestral inference in tumors: how much can we know?. *Journal of Theoretical Biology*, **2014**, 359, 136-45	2.3	6

13	Fine mapping--19th century style. *BMC Genetics*, **2005**, 6 Suppl 1, S63	2.6	6
12	Translating natural genetic variation to gene expression in a computational model of the Drosophila gap gene regulatory network. *PLoS ONE*, **2017**, 12, e0184657	3.7	5
11	Conservation of social effects (between two species of despite reversal of sexual dimorphism. *Ecology and Evolution*, **2017**, 7, 10031-10041	2.8	5
10	Towards the molecular characterization of disease: comparison of molecular and histological analysis of esophageal epithelia. *Journal of Gastrointestinal Surgery*, **2007**, 11, 1095-104	3.3	5
9	A survey of current Bayesian gene mapping methods. *Human Genomics*, **2004**, 1, 371-4	6.8	5
8	Genome-wide association mapping using mixed-models: application to GAW15 Problem 3. *BMC Proceedings*, **2007**, 1 Suppl 1, S164	2.3	4
7	Cladistic analysis of genotype data-application to GAW15 Problem 3. *BMC Proceedings*, **2007**, 1 Suppl 1, S125	2.3	2
6	al3c: high-performance software for parameter inference using Approximate Bayesian Computation. *Bioinformatics*, **2015**, 31, 3549-51	7.2	1
5	Exact likelihood-free Markov chain Monte Carlo for elliptically contoured distributions. *Statistical Applications in Genetics and Molecular Biology*, **2015**, 14, 317-32	1.2	1
4	Practical Implications of Coalescent Theory **2010**, 63-84		1
3	Early mutation bursts in colorectal tumors. *PLoS ONE*, **2017**, 12, e0172516	3.7	1
2	Simulation-based Bayesian Analysis of Complex Data **2015**, 47, 176-183		
1	Spatial Modeling of Multilocus Data **2005**, 471-487		